SEQUENCE LISTING

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YAMAGUCHI, Nozomi
MITSUI, Shinichi

<120> NOVEL SERINE PROTEASE BSSP2

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<140> 09/856,371
<141> 2001-05-21

<150> JP 10/347785
<151> 1998-11-20

<150> PCT/JP99/06475
<151> 1999-11-19

<160> 44

<170> PatentIn version 3.1

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agc gtg atg ctt ggc tcc cgg cac acg tgt ggg gcc tct gtg ttg gca       96
Ser Val Met Leu Gly Ser Arg His Thr Cys Gly Ala Ser Val Leu Ala
            20                  25                  30

cca cac tgg gta gtg act gct gcc cac tgc atg tac agt ttc agg ctg      144
Pro His Trp Val Val Thr Ala Ala His Cys Met Tyr Ser Phe Arg Leu
        35                  40                  45

tcc cgc cta tcc agc tgg cgg gtt cat gca ggg ctg gtc agc cat ggt      192
Ser Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Gly
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gct gtc cga caa cac cag gga act atg gtg gag aag atc att cct cat      240
Ala Val Arg Gln His Gln Gly Thr Met Val Glu Lys Ile Ile Pro His
65                  70                  75                  80

cct ttg tac agt gcc cag aac cat gac tat gat gtg gct ctg ctg cag      288
Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Gln
                85                  90                  95

ctc cgg aca cca atc aac ttc tca gac acc gtg gac gct gtg tgc ttg      336
Leu Arg Thr Pro Ile Asn Phe Ser Asp Thr Val Asp Ala Val Cys Leu
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            100                 105                 110

ccg gcc aag gag cag tac ttt cca tgg ggg tcg cag tgc tgg gtg tct      384
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        115                 120                 125

ggc tgg ggc cac acc gac ccc agc cat act cat agc tca gat aca ctg      432
Gly Trp Gly His Thr Asp Pro Ser His Thr His Ser Ser Asp Thr Leu
    130                 135                 140

cag gac aca atg gta ccc ctg ctc agc acc cac ctc tgc aac agc tca      480
Gln Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys Asn Ser Ser
145                 150                 155                 160

tgc atg tac agt ggg gca ctt aca cac cgc atg ttg tgt gct ggc tac      528
Cys Met Tyr Ser Gly Ala Leu Thr His Arg Met Leu Cys Ala Gly Tyr
                165                 170                 175

ctg gat gga agg gca gac gca tgc cag gga gac agc ggg gga ccc ctg      576
Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu
            180                 185                 190

gta tgt ccc agt ggt gac acg tgg cac ctt gta ggg gtg gtc agc tgg      624
Val Cys Pro Ser Gly Asp Thr Trp His Leu Val Gly Val Val Ser Trp
        195                 200                 205

ggt cgt ggc tgt gca gag ccc aat cgc cca ggt gtc tat gcc aag gta      672
Gly Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly Val Tyr Ala Lys Val
    210                 215                 220

gca gag ttc ctg gac tgg atc cat gac act gtg cag gtc cgc tag          717
Ala Glu Phe Leu Asp Trp Ile His Asp Thr Val Gln Val Arg
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Pro His Trp Val Val Thr Ala Ala His Cys Met Tyr Ser Phe Arg Leu
        35                  40                  45

Ser Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Gly
    50                  55                  60

Ala Val Arg Gln His Gln Gly Thr Met Val Glu Lys Ile Ile Pro His
65                  70                  75                  80

Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Gln
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85 90 95

Leu Arg Thr Pro Ile Asn Phe Ser Asp Thr Val Asp Ala Val Cys Leu
100 105 110

Pro Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser Gln Cys Trp Val Ser
115 120 125

Gly Trp Gly His Thr Asp Pro Ser His Thr His Ser Ser Asp Thr Leu
130 135 140

Gln Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys Asn Ser Ser
145 150 155 160

Cys Met Tyr Ser Gly Ala Leu Thr His Arg Met Leu Cys Ala Gly Tyr
165 170 175

Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu
180 185 190

Val Cys Pro Ser Gly Asp Thr Trp His Leu Val Gly Val Val Ser Trp
195 200 205

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ctgcaagagt cttgggcata tcaggcttac tcaacacaag gccgtgaatc tgtctgacat 180

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caagctcaac agatcccagg agtttgctca actctctgct agaccgggag gccttgtaga     240

ggaggc atg gaa gcc cag gta ggg ctt ctg tgg gtt agc gct aac tgt        288
       Met Glu Ala Gln Val Gly Leu Leu Trp Val Ser Ala Asn Cys
       -35                 -30                 -25

cct tct ggc cga att gtt tct ctc aaa tgt tct gag tgt ggg gca agg       336
Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu Cys Gly Ala Arg
    -20                 -15                 -10

cct ctg gct tct cga ata gtt ggc ggc caa gct gtg gct tct ggg cgc       384
Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val Ala Ser Gly Arg
-5              -1  1                   5                   10

tgg cca tgg caa gct agc gtg atg ctt ggc tcc cgg cac acg tgt ggg       432
Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg His Thr Cys Gly
            15                  20                  25

gcc tct gtg ttg gca cca cac tgg gta gtg act gct gcc cac tgc atg       480
Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala Ala His Cys Met
        30                  35                  40

tac agt ttc agg ctg tcc cgc cta tcc agc tgg cgg gtt cat gca ggg       528
Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg Val His Ala Gly
    45                  50                  55

ctg gtc agc cat ggt gct gtc cga caa cac cag gga act atg gtg gag       576
Leu Val Ser His Gly Ala Val Arg Gln His Gln Gly Thr Met Val Glu
60                  65                  70                  75

aag atc att cct cat cct ttg tac agt gcc cag aac cat gac tat gat       624
Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp
                80                  85                  90

gtg gct ctg ctg cag ctc cgg aca cca atc aac ttc tca gac acc gtg       672
Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe Ser Asp Thr Val
            95                  100                 105

gac gct gtg tgc ttg ccg gcc aag gag cag tac ttt cca tgg ggg tcg       720
Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser
        110                 115                 120

cag tgc tgg gtg tct ggc tgg ggc cac acc gac ccc agc cat act cat       768
Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro Ser His Thr His
    125                 130                 135

agc tca gat aca ctg cag gac aca atg gta ccc ctg ctc agc acc cac       816
Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu Leu Ser Thr His
140                 145                 150                 155

ctc tgc aac agc tca tgc atg tac agt ggg gca ctt aca cac cgc atg       864
Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu Thr His Arg Met
                160                 165                 170

ttg tgt gct ggc tac ctg gat gga agg gca gac gca tgc cag gga gac       912
Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp
            175                 180                 185

agc ggg gga ccc ctg gta tgt ccc agt ggt gac acg tgg cac ctt gta       960
Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr Trp His Leu Val
        190                 195                 200

ggg gtg gtc agc tgg ggt cgt ggc tgt gca gag ccc aat cgc cca ggt      1008
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Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly
    205                 210                 215

gtc tat gcc aag gta gca gag ttc ctg gac tgg atc cat gac act gtg      1056
Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr Val
220                 225                 230                 235

cag gtc cgc tagccgaaga agcagcagca gccacctgtg acgccgagct              1105
Gln Val Arg

gtggatcgcc catggatcac cccagtctgg gggccagcat ctgggtcact gggcctctcc    1165

ccaaaggctc tgacttcgag ttcatctttc tcatctgaga acctccacaa caggaaaagg    1225

agtctgcggc tagattggga atgatggtga gaggaaggga taggaggaca gaagagacag    1285

cagaggcttc tggaagcatc tgggagactg ctcctctgct ccccccacac cccacgtgca    1345

tccactgggg gatgctggag atgcccaatc cttgtttctt gtggggccac tggaaggcta    1405

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acaagctcag gtaaaggcac ggaagtcaag atcccctctc ccccgtgcgg tcctgttctg    1525

aggtaagcta atagccccgc accaggcaga ggtctacagg gtaagaagga tgcagttggg    1585

ctacacgacg ctatttttca aatgatgttt ctgtaaattg gttgagagag ttttgttatt    1645

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                -15                 -10                 -5

Ala Ser Arg Ile Val Gly Gly Gln Ala Val Ala Ser Gly Arg Trp Pro
        -1  1               5                   10

Trp Gln Ala Ser Val Met Leu Gly Ser Arg His Thr Cys Gly Ala Ser
    15                  20                  25

Val Leu Ala Pro His Trp Val Val Thr Ala Ala His Cys Met Tyr Ser
30                  35                  40                  45

Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val
                50                  55                  60
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Ser His Gly Ala Val Arg Gln His Gln Gly Thr Met Val Glu Lys Ile
            65                  70                  75

Ile Pro His Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala
        80                  85                  90

Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe Ser Asp Thr Val Asp Ala
    95                  100                 105

Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser Gln Cys
110                 115                 120                 125

Trp Val Ser Gly Trp Gly His Thr Asp Pro Ser His Thr His Ser Ser
                130                 135                 140

Asp Thr Leu Gln Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys
            145                 150                 155

Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu Thr His Arg Met Leu Cys
        160                 165                 170

Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly
    175                 180                 185

Gly Pro Leu Val Cys Pro Ser Gly Asp Thr Trp His Leu Val Gly Val
190                 195                 200                 205

Val Ser Trp Gly Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly Val Tyr
                210                 215                 220

Ala Lys Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr Val Gln Val
            225                 230                 235

Arg
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ccaatggaga ttcggtgcac ggaagagggt gctgggcctg ggatcttcag aatggagttg     180

ggagaccaga ggcaatccat ttctcagtcc caacgctggt gctgcctgca acgtggctgt     240

gtaatactgg gcgtcctggg gctgctggct ggagcaggca ttgcttcatg gctcttagtg     300

ttgtatctat ggccggctgc ctctccatcc atctctggga cgttgcagga ggaggagatg     360

actttgaact gtccaggagt gagctgtgag gaagagctcc ttccatctct tcccaaaaca     420

gaataaatgg aggggatctt ctgcttcaag tacaagtaag agctcggcca gactggctcc     480

tggtctgcca tgagggctgg agccccgccc tgggc atg cac atc tgc aag agt        533
                                        Met His Ile Cys Lys Ser
                                                    -70

ctt ggg cat atc agg ctt act caa cac aag gcc gtg aat ctg tct gac       581
Leu Gly His Ile Arg Leu Thr Gln His Lys Ala Val Asn Leu Ser Asp
        -65                 -60                 -55

atc aag ctc aac aga tcc cag gag ttt gct caa ctc tct gct aga ccg       629
Ile Lys Leu Asn Arg Ser Gln Glu Phe Ala Gln Leu Ser Ala Arg Pro
    -50                 -45                 -40

gga ggc ctt gta gag gag gca tgg aag ccc agc gct aac tgt cct tct       677
Gly Gly Leu Val Glu Glu Ala Trp Lys Pro Ser Ala Asn Cys Pro Ser
-35                 -30                 -25                 -20

ggc cga att gtt tct ctc aaa tgt tct gag tgt ggg gca agg cct ctg       725
Gly Arg Ile Val Ser Leu Lys Cys Ser Glu Cys Gly Ala Arg Pro Leu
                -15                 -10                 -5

gct tct cga ata gtt ggc ggc caa gct gtg gct tct ggg cgc tgg cca       773
Ala Ser Arg Ile Val Gly Gly Gln Ala Val Ala Ser Gly Arg Trp Pro
        -1  1                   5                   10

tgg caa gct agc gtg atg ctt ggc tcc cgg cac acg tgt ggg gcc tct       821
Trp Gln Ala Ser Val Met Leu Gly Ser Arg His Thr Cys Gly Ala Ser
    15                  20                  25

gtg ttg gca cca cac tgg gta gtg act gct gcc cac tgc atg tac agt       869
Val Leu Ala Pro His Trp Val Val Thr Ala Ala His Cys Met Tyr Ser
30                  35                  40                  45

ttc agg ctg tcc cgc cta tcc agc tgg cgg gtt cat gca ggg ctg gtc       917
Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val
                50                  55                  60

agc cat ggt gct gtc cga caa cac cag gga act atg gtg gag aag atc       965
Ser His Gly Ala Val Arg Gln His Gln Gly Thr Met Val Glu Lys Ile
            65                  70                  75

att cct cat cct ttg tac agt gcc cag aac cat gac tat gat gtg gct      1013
Ile Pro His Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala
        80                  85                  90
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ctg ctg cag ctc cgg aca cca atc aac ttc tca gac acc gtg gac gct      1061
Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe Ser Asp Thr Val Asp Ala
    95                  100                 105

gtg tgc ttg ccg gcc aag gag cag tac ttt cca tgg ggg tcg cag tgc      1109
Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser Gln Cys
110                 115                 120                 125

tgg gtg tct ggc tgg ggc cac acc gac ccc agc cat act cat agc tca      1157
Trp Val Ser Gly Trp Gly His Thr Asp Pro Ser His Thr His Ser Ser
                130                 135                 140

gat aca ctg cag gac aca atg gta ccc ctg ctc agc acc cac ctc tgc      1205
Asp Thr Leu Gln Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys
            145                 150                 155

aac agc tca tgc atg tac agt ggg gca ctt aca cac cgc atg ttg tgt      1253
Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu Thr His Arg Met Leu Cys
        160                 165                 170

gct ggc tac ctg gat gga agg gca gac gca tgc cag gga gac agc ggg      1301
Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly
    175                 180                 185

gga ccc ctg gta tgt ccc agt ggt gac acg tgg cac ctt gta ggg gtg      1349
Gly Pro Leu Val Cys Pro Ser Gly Asp Thr Trp His Leu Val Gly Val
190                 195                 200                 205

gtc agc tgg ggt cgt ggc tgt gca gag ccc aat cgc cca ggt gtc tat      1397
Val Ser Trp Gly Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly Val Tyr
                210                 215                 220

gcc aag gta gca gag ttc ctg gac tgg atc cat gac act gtg cag gtc      1445
Ala Lys Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr Val Gln Val
            225                 230                 235

cgc tagccgaaga agcagcagca gccacctgtg acgccgagct gtggatcgcc           1498
Arg
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catggatcac cccagtctgg gggccagcat ctgggtcact gggcctctcc ccaaaggctc   1558

tgacttcgag ttcatctttc tcatctgaga acctccacaa caggaaaagg agtctgcggc   1618

tagattggga atgatggtga gaggaaggga taggaggaca gaagagacag cagaggcttc   1678

tggaagcatc tgggagactg ctcctctgct ccccccacac cccacgtgca tccactgggg   1738

gatgctggag atgcccaatc cttgtttctt gtggggccac tggaaggcta agtccaactt   1798

tagaggatgc cctgtctcga gagttactag gcagataagg ttaaggttgg acaagctcag   1858

gtaaaggcac ggaagtcaag atcccctctc ccccgtgcgg tcctgttctg aggtaagcta   1918

atagccccgc accaggcaga ggtctacagg gtaagaagga tgcagttggg ctacacgacg   1978

ctatttttca aatgatgttt ctgtaaattg gttgagagag ttttgttatt aaacagaaat   2038

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Ala Val Asn Leu Ser Asp Ile Lys Leu Asn Arg Ser Gln Glu Phe Ala
        -55                 -50                 -45

Gln Leu Ser Ala Arg Pro Gly Gly Leu Val Glu Glu Ala Trp Lys Pro
    -40                 -35                 -30

Ser Ala Asn Cys Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu
-25                 -20                 -15                 -10

Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val
                -5                  -1  1                   5

Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg
        10                  15                  20

His Thr Cys Gly Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala
    25                  30                  35

Ala His Cys Met Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg
40                  45                  50                  55

Val His Ala Gly Leu Val Ser His Gly Ala Val Arg Gln His Gln Gly
                60                  65                  70

Thr Met Val Glu Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn
            75                  80                  85

His Asp Tyr Asp Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe
        90                  95                  100

Ser Asp Thr Val Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe
    105                 110                 115

Pro Trp Gly Ser Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro
120                 125                 130                 135

Ser His Thr His Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu
                140                 145                 150

Leu Ser Thr His Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu
            155                 160                 165
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```
Thr His Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala
        170                 175                 180

Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr
    185                 190                 195

Trp His Leu Val Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro
200                 205                 210                 215

Asn Arg Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile
                220                 225                 230

His Asp Thr Val Gln Val Arg
            235
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gctggatctt caaccactat ttctccagag tccaacactg gatgaccaaa gccca atg      118
                                                              Met

gag att  cgg tgc acg gaa gag  ggt gct ggg cct ggg  atc ttc aga        163
Glu Ile  Arg Cys Thr Glu Glu  Gly Ala Gly Pro Gly  Ile Phe Arg
    -205                -200                -195

atg gag  ttg gga gac cag agg  caa tcc att tct cag  tcc caa cgc        208
Met Glu  Leu Gly Asp Gln Arg  Gln Ser Ile Ser Gln  Ser Gln Arg
    -190                -185                -180

tgg tgc  tgc ctg caa cgt ggc  tgt gta ata ctg ggc  gtc ctg ggg        253
Trp Cys  Cys Leu Gln Arg Gly  Cys Val Ile Leu Gly  Val Leu Gly
    -175                -170                -165

ctg ctg  gct gga gca ggc att  gct tca tgg ctc tta  gtg ttg tat        298
Leu Leu  Ala Gly Ala Gly Ile  Ala Ser Trp Leu Leu  Val Leu Tyr
    -160                -155                -150

cta tgg  cca gct gcc tct cca  tcc atc tct ggg acg  ttg cag gag        343
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Leu Trp  Pro Ala Ala Ser Pro  Ser Ile Ser Gly Thr  Leu Gln Glu
    -145                  -140                  -135

gag gag  atg act ttg aac tgt  cca gga gtg agc tgt  gag gaa gag      388
Glu Glu  Met Thr Leu Asn Cys  Pro Gly Val Ser Cys  Glu Glu Glu
    -130                  -125                  -120

ctc ctt  cca tct ctt ccc aaa  aca gta tct ttc aga  ata aat gga      433
Leu Leu  Pro Ser Leu Pro Lys  Thr Val Ser Phe Arg  Ile Asn Gly
    -115                  -110                  -105

gag gat  ctt ctg ctt caa gta caa gta aga gct cgg cca gac tgg ctc  481
Glu Asp  Leu Leu Leu Gln Val Gln Val Arg Ala Arg Pro Asp Trp Leu
    -100                  -95                   -90

ctg gtc tgc cat gag ggc tgg agc ccc gcc ctg ggc atg cac atc tgc  529
Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly Met His Ile Cys
-85                   -80                   -75                   -70

aag agt ctt ggg cat atc agg ctt act caa cac aag gcc gtg aat ctg  577
Lys Ser Leu Gly His Ile Arg Leu Thr Gln His Lys Ala Val Asn Leu
                  -65                   -60                   -55

tct gac atc aag ctc aac aga tcc cag gag ttt gct caa ctc tct gct  625
Ser Asp Ile Lys Leu Asn Arg Ser Gln Glu Phe Ala Gln Leu Ser Ala
            -50                   -45                   -40

aga ccg gga ggc ctt gta gag gag gca tgg aag ccc agc gct aac tgt  673
Arg Pro Gly Gly Leu Val Glu Glu Ala Trp Lys Pro Ser Ala Asn Cys
        -35                   -30                   -25

cct tct ggc cga att gtt tct ctc aaa tgt tct gag tgt ggg gca agg  721
Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu Cys Gly Ala Arg
    -20                   -15                   -10

cct ctg gct tct cga ata gtt ggc ggc caa gct gtg gct tct ggg cgc  769
Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val Ala Ser Gly Arg
-5               -1  1                 5                  10

tgg cca tgg caa gct agc gtg atg ctt ggc tcc cgg cac acg tgt ggg  817
Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg His Thr Cys Gly
            15                  20                  25

gcc tct gtg ttg gca cca cac tgg gta gtg act gct gcc cac tgc atg  865
Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala Ala His Cys Met
        30                  35                  40

tac agt ttc agg ctg tcc cgc cta tcc agc tgg cgg gtt cat gca ggg  913
Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg Val His Ala Gly
    45                  50                  55

ctg gtc agc cat ggt gct gtc cga caa cac cag gga act atg gtg gag  961
Leu Val Ser His Gly Ala Val Arg Gln His Gln Gly Thr Met Val Glu
60                  65                  70                  75

aag atc att cct cat cct ttg tac agt gcc cag aac cat gac tat gat 1009
Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp
                80                  85                  90

gtg gct ctg ctg cag ctc cgg aca cca atc aac ttc tca gac acc gtg 1057
Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe Ser Asp Thr Val
            95                  100                 105
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gac gct gtg tgc ttg ccg gcc aag gag cag tac ttt cca tgg ggg tcg     1105
Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser
        110                 115                 120

cag tgc tgg gtg tct ggc tgg ggc cac acc gac ccc agc cat act cat     1153
Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro Ser His Thr His
    125                 130                 135

agc tca gat aca ctg cag gac aca atg gta ccc ctg ctc agc acc cac     1201
Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu Leu Ser Thr His
140                 145                 150                 155

ctc tgc aac agc tca tgc atg tac agt ggg gca ctt aca cac cgc atg     1249
Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu Thr His Arg Met
                160                 165                 170

ttg tgt gct ggc tac ctg gat gga agg gca gac gca tgc cag gga gac     1297
Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp
            175                 180                 185

agc ggg gga ccc ctg gta tgt ccc agt ggt gac acg tgg cac ctt gta     1345
Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr Trp His Leu Val
        190                 195                 200

ggg gtg gtc agc tgg ggt cgt ggc tgt gca gag ccc aat cgc cca ggt     1393
Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly
    205                 210                 215

gtc tat gcc aag gta gca gag ttc ctg gac tgg atc cat gac act gtg     1441
Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr Val
220                 225                 230                 235

cag gtc cgc tagccgaaga agcagcagca gccacctgtg acgccgagct             1490
Gln Val Arg
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gtggatcgcc catggatcac cccagtctgg gggccagcat ctgggtcact gggcctctcc   1550

ccaaaggctc tgacttcgag ttcatctttc tcatctgaga acctccacaa caggaaaagg   1610

agtctgcggc tagattggga atgatggtga gaggaaggga taggaggaca gaagagacag   1670

cagaggcttc tggaagcatc tgggagactg ctcctctgct ccccccacac cccacgtgca   1730

tccactgggg gatgctggag atgcccaatc cttgtttctt gtggggccac tggaaggcta   1790

agtccaactt tagaggatgc cctgtctcga gagttactag gcagataagg ttaaggttgg   1850

acaagctcag gtaaaggcac ggaagtcaag atcccctctc ccccgtgcgg tcctgttctg   1910

aggtaagcta atagccccgc accaggcaga ggtctacagg gtaagaagga tgcagttggg   1970

ctacacgacg ctatttttca aatgatgttt ctgtaaattg gttgagagag ttttgttatt   2030

aaacagaaat tatgtataaa aaaaaaaaaa aaaaaaaaaa                         2070
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<210> 8
<211> 445
<212> PRT
<213> Mus sp.

<400> 8

Met Glu Ile Arg Cys Thr Glu Glu Gly Ala Gly Pro Gly Ile Phe
-205 -200 -195

Arg Met Glu Leu Gly Asp Gln Arg Gln Ser Ile Ser Gln Ser Gln
-190 -185 -180

Arg Trp Cys Cys Leu Gln Arg Gly Cys Val Ile Leu Gly Val Leu
-175 -170 -165

Gly Leu Leu Ala Gly Ala Gly Ile Ala Ser Trp Leu Leu Val Leu
-160 -155 -150

Tyr Leu Trp Pro Ala Ala Ser Pro Ser Ile Ser Gly Thr Leu Gln
-145 -140 -135

Glu Glu Glu Met Thr Leu Asn Cys Pro Gly Val Ser Cys Glu Glu
-130 -125 -120

Glu Leu Leu Pro Ser Leu Pro Lys Thr Val Ser Phe Arg Ile Asn
-115 -110 -105

Gly Glu Asp Leu Leu Leu Gln Val Gln Val Arg Ala Arg Pro Asp Trp
-100 -95 -90

Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly Met His Ile
-85 -80 -75

Cys Lys Ser Leu Gly His Ile Arg Leu Thr Gln His Lys Ala Val Asn
-70 -65 -60 -55

Leu Ser Asp Ile Lys Leu Asn Arg Ser Gln Glu Phe Ala Gln Leu Ser
-50 -45 -40

Ala Arg Pro Gly Gly Leu Val Glu Glu Ala Trp Lys Pro Ser Ala Asn
-35 -30 -25

Cys Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu Cys Gly Ala
-20 -15 -10

Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val Ala Ser Gly
-5 -1 1 5 10

Arg Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg His Thr Cys
15 20 25

Gly Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala Ala His Cys
30 35 40

Met Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg Val His Ala
45 50 55

Gly Leu Val Ser His Gly Ala Val Arg Gln His Gln Gly Thr Met Val
60 65 70

Glu Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr
75 80 85 90

Asp Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe Ser Asp Thr
95 100 105

Val Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe Pro Trp Gly
110 115 120

Ser Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro Ser His Thr
125 130 135

His Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu Leu Ser Thr
140 145 150

His Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu Thr His Arg
155 160 165 170

Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly
175 180 185

Asp Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr Trp His Leu
190 195 200

Val Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro Asn Arg Pro
205 210 215

Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr
220 225 230

Val Gln Val Arg
235

<210> 9
<211> 2265
<212> DNA
<213> Homo sapiens

<220>
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<222> (156)..(1526)
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<400> 9

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tgctgggctt gcatttaatc aatgcatggc cagagaacag gagcggaaca ttgcctagta    120

gaccctgagg ctttacaaca gtgctactga ccccct atg agc ctg  atg ctg gat      173
                                        Met Ser Leu  Met Leu Asp
                                             -215

gac caa  ccc cct atg gag gcc  cag tat gca gag gag  ggc cca gga        218
Asp Gln  Pro Pro Met Glu Ala  Gln Tyr Ala Glu Glu  Gly Pro Gly
    -210                 -205                 -200

cct ggg  atc ttc aga gca gag  cct gga gac cag cag  cat ccc att        263
Pro Gly  Ile Phe Arg Ala Glu  Pro Gly Asp Gln Gln  His Pro Ile
    -195                 -190                 -185

tct cag  gcg gtg tgc tgg cgt  tcc atg cga cgt ggc  tgt gca gtg        308
Ser Gln  Ala Val Cys Trp Arg  Ser Met Arg Arg Gly  Cys Ala Val
    -180                 -175                 -170

ctg gga  gcc ctg ggg ctg ctg  gcc ggt gca ggt gtt  ggc tca tgg        353
Leu Gly  Ala Leu Gly Leu Leu  Ala Gly Ala Gly Val  Gly Ser Trp
    -165                 -160                 -155

ctc cta  gtg ctg tat ctg tgt  cct gct gcc tct cag  ccc att tcc        398
Leu Leu  Val Leu Tyr Leu Cys  Pro Ala Ala Ser Gln  Pro Ile Ser
    -150                 -145                 -140

ggg acc  ttg cag gat gag gag  ata act ttg agc tgc  tca gag gcc        443
Gly Thr  Leu Gln Asp Glu Glu  Ile Thr Leu Ser Cys  Ser Glu Ala
    -135                 -130                 -125

agc gct  gag gaa gct ctg ctc  cct gca ctc ccc aaa  aca gta tct        488
Ser Ala  Glu Glu Ala Leu Leu  Pro Ala Leu Pro Lys  Thr Val Ser
    -120                 -115                 -110

ttc aga  ata aac agc gaa gac  ttc ttg ctg gaa gcg caa gtg agg gat    536
Phe Arg  Ile Asn Ser Glu Asp  Phe Leu Leu Glu Ala Gln Val Arg Asp
    -105                 -100                 -95

cag cca cgc tgg ctc ctg gtc tgc cat gag ggc tgg agc ccc gcc ctg      584
Gln Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu
-90                  -85                  -80                  -75

ggg ctg cag atc tgc tgg agc ctt ggg cat ctc aga ctc act cac cac      632
Gly Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His
                -70                  -65                  -60

aag gga gta aac ctc act gac atc aaa ctc aac agt tcc cag gag ttt      680
Lys Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe
            -55                  -50                  -45

gct cag ctc tct cct aga ctg gga ggc ttc ctg gag gag gcg tgg cag      728
Ala Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln
```

```
        -40                 -35                 -30

ccc agg aac aac tgc act tct ggt caa gtt gtt tcc ctc aga tgc tct      776
Pro Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser
    -25                 -20                 -15

gag tgt gga gcg agg ccc ctg gct tcc cgg ata gtt ggt ggg cag tct      824
Glu Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser
-10                 -5                  -1  1                   5

gtg gct cct ggg cgc tgg ccg tgg cag gcc agc gtg gcc ctg ggc ttc      872
Val Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe
            10                  15                  20

cgg cac acg tgt ggg ggc tct gtg cta gcg cca cgc tgg gtg gtg act      920
Arg His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr
        25                  30                  35

gct gca cat tgt atg cac agt ttc agg ctg gcc cgc ctg tcc agc tgg      968
Ala Ala His Cys Met His Ser Phe Arg Leu Ala Arg Leu Ser Ser Trp
    40                  45                  50

cgg gtt cat gcg ggg ctg gtc agc cac agt gcc gtc agg ccc cac caa     1016
Arg Val His Ala Gly Leu Val Ser His Ser Ala Val Arg Pro His Gln
55                  60                  65                  70

ggg gct ctg gtg gag agg att atc cca cac ccc ctc tac agt gcc cag     1064
Gly Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln
                75                  80                  85

aat cat gac tac gac gtc gcc ctc ctg agg ctc cag acc gct ctc aac     1112
Asn His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn
            90                  95                  100

ttc tca gac act gtg ggc gct gtg tgc ctg ccg gcc aag gaa cag cat     1160
Phe Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His
        105                 110                 115

ttt ccg aag ggc tcg cgg tgc tgg gtg tct ggc tgg ggc cac acc cac     1208
Phe Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His
    120                 125                 130

cct agc cat act tac agc tcg gat atg ctc cag gac acg gtg gtg ccc     1256
Pro Ser His Thr Tyr Ser Ser Asp Met Leu Gln Asp Thr Val Val Pro
135                 140                 145                 150

ttg ttc agc act cag ctc tgc aac agc tct tgc gtg tac agc gga gcc     1304
Leu Phe Ser Thr Gln Leu Cys Asn Ser Ser Cys Val Tyr Ser Gly Ala
                155                 160                 165

ctc acc ccc cgc atg ctt tgc gct ggc tac ctg gac gga agg gct gat     1352
Leu Thr Pro Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp
            170                 175                 180

gca tgc cag gga gat agc ggg ggc ccc cta gtg tgc cca gat ggg gac     1400
Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Asp Gly Asp
        185                 190                 195

aca tgg cgc cta gtg ggg gtg gtc agc tgg ggg cgt gcg tgc gca gag     1448
Thr Trp Arg Leu Val Gly Val Val Ser Trp Gly Arg Ala Cys Ala Glu
    200                 205                 210

ccc aat cac cca ggt gtc tac gcc aag gta gct gag ttt ctg gac tgg     1496
```

```
Pro Asn His Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp
215                 220                 225                 230

atc cat gac act gct cag gac tcc ctc ctc tgagtcctgc tgtttcctcc      1546
Ile His Asp Thr Ala Gln Asp Ser Leu Leu
                235                 240

agtctcactg cacaccactg cctcatgctt cctggggcct ccagcagctc cactaatgga  1606

ggagaggcag tagcctccga cacagaacgc atggacctcc tactactgtg tgtgaggaac  1666

agtcactacc cactggccag ccacccagcc aacaggtctc tcctcttggg ccctgatttc  1726

agagtcctct ttctcactag agactcaatg acagaagaga ggctgggact tggttgggca  1786

tgctgtggtt gctgagggat gaggggggagg agagaggtag gagctggaga tgaagagact  1846

gctagaagca gcaggaagcc tgcccttctg ccctctcccc tccctgcccc tgtgtgagtc  1906

ttttagggag ggtgactggg aggtgccccc cgtcccacct ttttcctgtg ctctaggtgg  1966

gctaagtgcc tccctagagg actccatggc tgagaggctc ctgggcagat ggggtcaagg  2026

ctgggccagt cccagatgaa gcctatggga gtcaggaccc tctccactct ccctctccac  2086

tccccttcct gttctcacct ggctgtggct ggccctgtgt ggggtgggta cactggaaaa  2146

caagaaggtt ggagttggtc taggacattg gttttaaatg acagttctgt gaactggtcc  2206

aaggaggttc tgttattaaa gtgatatatg gtcttgaaaa aaaaaaaaaa aaaaaaaaa   2265
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<210> 10
<211> 457
<212> PRT
<213> Homo sapiens

<400> 10

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Met Ser Leu  Met Leu Asp Asp Gln  Pro Pro Met Glu Ala  Gln Tyr
        -215                -210                -205

Ala Glu Glu  Gly Pro Gly Pro Gly  Ile Phe Arg Ala Glu  Pro Gly
        -200                -195                -190

Asp Gln Gln  His Pro Ile Ser Gln  Ala Val Cys Trp Arg  Ser Met
        -185                -180                -175

Arg Arg Gly  Cys Ala Val Leu Gly  Ala Leu Gly Leu Leu  Ala Gly
        -170                -165                -160

Ala Gly Val  Gly Ser Trp Leu Leu  Val Leu Tyr Leu Cys  Pro Ala
        -155                -150                -145

Ala Ser Gln  Pro Ile Ser Gly Thr  Leu Gln Asp Glu Glu  Ile Thr
        -140                -135                -130
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```
Leu Ser Cys  Ser Glu Ala Ser Ala  Glu Glu Ala Leu Leu  Pro Ala
        -125                 -120                 -115

Leu Pro Lys  Thr Val Ser Phe Arg  Ile Asn Ser Glu Asp  Phe Leu
        -110                 -105                 -100

Leu Glu Ala Gln Val Arg Asp Gln Pro Arg Trp Leu Leu Val Cys His
        -95                  -90                  -85

Glu Gly Trp Ser Pro Ala Leu Gly Leu Gln Ile Cys Trp Ser Leu Gly
    -80                  -75                  -70

His Leu Arg Leu Thr His His Lys Gly Val Asn Leu Thr Asp Ile Lys
-65                  -60                  -55                  -50

Leu Asn Ser Ser Gln Glu Phe Ala Gln Leu Ser Pro Arg Leu Gly Gly
                -45                  -40                  -35

Phe Leu Glu Glu Ala Trp Gln Pro Arg Asn Asn Cys Thr Ser Gly Gln
            -30                  -25                  -20

Val Val Ser Leu Arg Cys Ser Glu Cys Gly Ala Arg Pro Leu Ala Ser
        -15                  -10                  -5

Arg Ile Val Gly Gly Gln Ser Val Ala Pro Gly Arg Trp Pro Trp Gln
-1  1                5                   10                  15

Ala Ser Val Ala Leu Gly Phe Arg His Thr Cys Gly Gly Ser Val Leu
                20                  25                  30

Ala Pro Arg Trp Val Val Thr Ala Ala His Cys Met His Ser Phe Arg
            35                  40                  45

Leu Ala Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His
        50                  55                  60

Ser Ala Val Arg Pro His Gln Gly Ala Leu Val Glu Arg Ile Ile Pro
    65                  70                  75

His Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu
80                  85                  90                  95

Arg Leu Gln Thr Ala Leu Asn Phe Ser Asp Thr Val Gly Ala Val Cys
                100                 105                 110

Leu Pro Ala Lys Glu Gln His Phe Pro Lys Gly Ser Arg Cys Trp Val
            115                 120                 125
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Ser Gly Trp Gly His Thr His Pro Ser His Thr Tyr Ser Ser Asp Met
130 135 140

Leu Gln Asp Thr Val Val Pro Leu Phe Ser Thr Gln Leu Cys Asn Ser
145 150 155

Ser Cys Val Tyr Ser Gly Ala Leu Thr Pro Arg Met Leu Cys Ala Gly
160 165 170 175

Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro
180 185 190

Leu Val Cys Pro Asp Gly Asp Thr Trp Arg Leu Val Gly Val Val Ser
195 200 205

Trp Gly Arg Ala Cys Ala Glu Pro Asn His Pro Gly Val Tyr Ala Lys
210 215 220

Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr Ala Gln Asp Ser Leu
225 230 235

Leu
240

<210> 11
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide to construct plasmid pSecTrypHis

<400> 11
aagcttggct agcaacacca tgaatctact cctgatcctt acctttgttg ctgctgctgt 60

tgctgccccc tttgacgacg atgacaagga tccgaattc 99

<210> 12
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
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<223> Designed oligonucleotide to construct plasmid pSecTrypHis

<400> 12
gaattcggat ccttgtcatc gtcgtcaaag ggggcagcaa cagcagcagc aacaaaggta 60

aggatcagga gtagattcat ggtgttgcta gccaagctt 99

<210> 13
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer t amplify neurosin-encoding seque
nce

<400> 13
ttggtgcatg gcgga 15

<210> 14
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer to amplify neurosin-encoding sequ
ence

<400> 14
tcctcgagac ttggcctgaa tggtttt 27

<210> 15
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer to amplify a portion of plasmid p
SecTrypHis/Neurosin

<400> 15
gcgctagcag atctccatga atctactcct gatcc 35

<210> 16

<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer to amplify a portion of plasmid p SecTrypHis/Neurosin

<400> 16
tgaagcttgc catggaccaa cttgtcatc 29

<210> 17
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer to amplify a portion of plasmid p TrypHis

<400> 17
ccaagcttca ccatcaccat caccat 26

<210> 18
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer to amplify a portion of plasmid p TrypSigTag

<400> 18
gcacagtcga ggctgat 17

<210> 19
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature

<223> Designed oligonucleotide primer to amplify a portion of plasmid p
FBTrypSigTag

<400> 19
caaatgtggt atggctg 17

<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer to amplify conserved region of se
rin proteases-encoding sequence

<220>
<221> misc_feature
<222> (9)..(9)
<223> n is a, c, g or t.

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g or t.

<400> 20
gtgctcacng cngcbcaytg 20

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer to amplify conserved region of se
rin proteases-encoding sequence

<220>
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<222> (12)..(12)
<223> n is a, c, g or t.

<220>
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<223> n is a, c, g or t.

<400> 21
ccvctrwsdc cnccnggcga 20

<210> 22
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as mBSSP2.0 for RACE f
or mBSSP2 (forward)

<400> 22
atggtggaga agatcattcc t 21

<210> 23
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as mBSSP2.1 for RACE f
or mBSSP2 (forward)

<400> 23
tacagtgccc agaaccatg 19

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as mBSSPF4 for RACE fo
r mBSSP2 (forward)

<400> 24
ctcaactctc tgctagaccg 20

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as mBSSP2F5 toamplify mature mBSSP2-encoding region (forward)

<400> 25
atagttggcg gccaagctgt 20

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as mBSSP2.2 for RACE f or mBSSP2 (reverse)

<400> 26
cccagcagaa cttactgcct 20

D1 Cont.

<210> 27
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as mBSSP2E2 for RACE f or mBSSP2 (reverse)

<400> 27
tgttgcagag gtgggtgctg 20

<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as mBSSP2R2 for RACE f or mBSSP2 (reverse)

<400> 28
taccattgtg tcctgcagtg t 21

<210> 29
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as mBSSP2R5/E to amplify full-length mBSSP2-encoding mRNA (reverse)

<400> 29
tgaattctgc tgcttcttcg gctagcg 27

<210> 30
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as BSSP2SPF to amplify a portion of hBSSP2 (forward)

<400> 30
actgctgccc actgcatg 18

<210> 31
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as BSSP2SPR to amplify a portion of hBSSP2 (reverse)

<400> 31
caggggtccc ccgctgtctc c 21

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as hBSSP2F11 for RACE for hBSSP2 (forward)

<400> 32
gctctcaact tctcagacac 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as hBSSP2R12 for RACE for hBSSP2 (reverse)

<400> 33
actcagctac cttggcgtag 20

D' Cont.

<210> 34
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as hBSSP2R11 for RACE for hBSSP2 (reverse)

<400> 34
cctggagcat atccgagctg 20

<210> 35
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as hBSSP2F12 to amplify full length hBSSP2 (forward)

<400> 35
gctttacaac agtgctac 18

<210> 36
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as hBSSP2R13/E to amplify full length hBSSP2 (reverse)

<400> 36
tggaattcga ggaaacagca ggactcag 28

<210> 37
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer for RACE for hBSSP2

<400> 37
tactagtcga cgcgtggcc 19

<210> 38
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as hBSSP2F13 to amplify a portion of hBSSP2 (forward)

<400> 38
actgctgccc actgcatg 18

<210> 39
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide primer designated as FBTrpsigtagF5 to de
tect hBSSP2

<400> 39
gcgctagcag atctccatga atctactcct gatcc 35

<210> 40
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide to construct plasmid pTrypHis

<400> 40
aagcttggct agcaacacca tgaatctact cctgatcctt acctttgttg ctgctgctgt 60

tgctgccccc tttcaccatc accatcacca tgacgacgat gacaaggatc cgaattc 117

<210> 41
<211> 117
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<223> Designed oligonucleotide to construct plasmid pTrypHis

<400> 41
gaattcggat ccttgtcatc gtcgtcatgg tgatggtgat ggtgaaaggg ggcagcaaca 60

gcagcagcaa caaaggtaag gatcaggagt agattcatgg tgttgctagc caagctt 117

<210> 42
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 42

Asp Asp Asp Asp Lys
1 5

<210> 43
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 43

Leu Val His Gly
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<210> 44
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 44
ggccacgcgt cgactagtac ttttttttt tttttt 37